

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 98597

TO: Phillip Gambel Location: 8b03 / 9e12 Monday, July 14, 2003

Art Unit: 1644 Phone: 308-3997

Serial Number: 09 / 825580

From: Jan Delaval

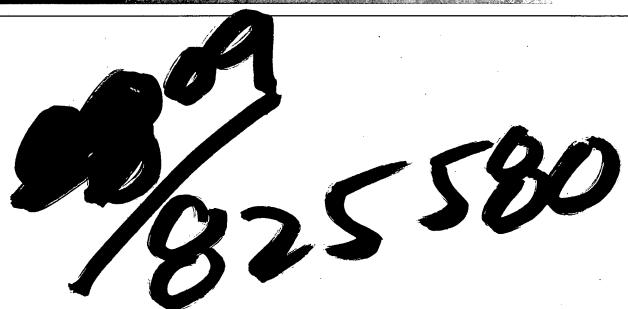
**Location: Biotech-Chem Library** 

CM1-1E07

Phone: 308-4498

jan.delaval@uspto.gov

### Search Notes



Jan Delaval Reference Librarian Biotechnology & Chemical Library CM1 1E07 – 703-308-4498 jan.delaval@uspto.gov



# 

### Delaval, Jan

From:

Sent: To:

Gambel, Phillip Sunday, July 13, 2003 9:36 AM Delaval, Jan 09 / 825580 eppihimer amd

Subject:

jan

please perform a sequence and a sequence interference search for

09 / 825,580 (eppihimer amd)

SEQ ID NO: 2

thanx

phillip gambel art unit 1644 308-3997

1644 mailbox 9e12

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Access 08# 98597

### SEARCH REQUEST FORM

### Scientific and Technical Information Center!

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	chone santibles 20	Senal Yumber	
Mail Box and Bidg/Roo	m Location:	Results Format Preferred (circle):	PAPER DISK E-MAIL
f more than one searc	h is submitted, please	prioritize searches in order of ne	ed.
tility of the invention Defit	with the full cas, Keywords, Synony	describe as specifically as possible the subjects, and registry numbers, and cospecial meaning. Give examples or relevant aims, and abstract.	
Fitle of Invention:			
nventors (please provide fo	ill names):		
Earliest Priority Filing D	ate		
h .		ormation (parent, child, divisional, or issued par	

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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searchera_	NA Sequence (#)	STN
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Centa Prepiring	Patent Family	WWW (nieme)
<u> </u>	Diher	Other (specify)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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CM protein - protein search, using sw model

July 14, 2003, 06:10:58; Search time 41 Seconds (without alignments) 942.586 Million cell updates/sec Run on:

US-09-825-580-2
2030
1 MPLQLLLLLLLLLGPGNSLQL.....TPEPREDREGDDLTLHSFLP 402 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

seq length: 0 seq length: 200000000 08 08 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	αı	Description
	2015	99.3	412	7	A57468	P-selectin glycopr
~	288.5	14.2	307	-	GSFF3	salivary glue prot
m	283	13.9	867	~	T45463	
4	271.5	13.4	998	N	T45462	
2	256	12.6	750	~	T42614	probable envelope
φ	250.5	12.3	797	-	VGBEX1	glycoprotein X pre
7	226.5	11.2	801	N	T29018	
80	210.5	10.4	825	~	T29634	
6	205.5	10.1	1151	~	T18535	10
10	204.5	10.1	770	~	T22808	hypothetical prote
11	198	9.8	3191	N	T22945	hypothetical prote
12	194.5		507		T44768	antifreeze glycope
13	194	٠	1161		S57180	probable membrane
14	193.5	9.5	196		T21460	hypothetical prote
15	193	9.5	658		T41309	
16	190	9.4	2761		T21064	hypothetical prote
17	189.5	9.3	3570	7	T45025	
18	188.5	9.3	1229	~	T25697	hypothetical prote
19	188.5	•	1829	~	T24583	hypothetical prote
20	187	•	1367	-	S48478	glucan 1,4-alpha-g
21	186.5		3020	~	A43932	mucin 2 precursor,
22	186		402	7	E86185	hypothetical prote
23	184	9.1	662	~	A45155	П
24	183		1777	~	T34369	hypothetical prote
25	182.5	-	851	~	T22696	
26	182.5	•	1832	~	T31113	mucin-like glycopr
27	181	•	235	~	PC2022	mucin like protein
28	180.5	8 6.9	400	Н	817	spasmolysin precur
50	180.5	6.8	839	N	F75518	

hypothetical prote	salivary glue prot	mucin - rat	mucin 5AC (clone J	US4 protein - huma	hypothetical prote	larval glue protei	mucin, tracheal (A	chitinase (EC 3.2.	mucin - rhesus mac	hypothetical prote	hypothetical prote	mucin 3 - human (f	zonadhesin - mouse	microfilarial shea	mucin 3 T10 - huma
T34513	801359	S24169	S53363	C43674	T21700	A60095	A37232	JC4566	151920	T26063	870305	PC4395	T42215	T46740	PC4397
0	N	~	N	7	~	~	~	N	N	N	~	7	~	<b>N</b>	7
3507	328	292	279	669	846	232	294	860	216	2225	792	648	5376	354	246
6.0	8.8	8.8	8.7	8.7	9.6	9.8			8	8.5	8.4	8.4	8.4	8.4	8.4
180	179.5	178	176.5	176.5	175	174.5	173.5	173.5	173	173	171.5	171	171	170.5	170

# ALIGNMENTS

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A57468
P-selectin glycoprotein ligand PSGL-1 precursor, long splice form - human
N;Contains: P-selectin glycoprotein ligand PSGL-1, long splice form; P-selectin glycopro
                                                                                                                 C;Species: Foretectin 94yourcein 119900 rSub-1, long splice form; P-selectin glycopro C;Species: Homo sapiens (man)
C;Date: 08-Dec-1995 #sequence revision 08-Dec-1995 #text_change 08-Oct-1999
C;Accession: A57468; A49267; A54711
R;Veldman, G.M.; Bean, K.M.; Cumming, D.A.; Eddy, R.L.; Sait, S.N.J.; Shows, T.B.
A;Title: Genomic organization and chromosomal localization of the gene encoding human P-A;Reference number: A57468; MUID:95332364; PMID:7541799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-412 - VNED.
A; Residues: 1-412 - VNED.
A; CTOSB-referencies: GB: UD5955
R; Sako, D; Chang, X.J.; Barone, K.M.; Vachino, G.; White, H.M.; Shaw, G.; Veldman, G.M
CELI 75, 1179-1186, 1193
A; Title: Expression cloning of a functional glycoprotein ligand for P-selectin.
A; Reference number: A49267; MUID: 94084793; PMID: 7505206
```

A; Accession: A49267

A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Molecule type: mSNA
A;Cross.references: 08:U02297; NID:9435416; PIDN:AAC50061.1; PID:9435417
B;Moore, K.L.; Eaton, S.F.; Lyons, D.E.; Lichenstein, H.S.; Cummings, R.D.; McEver, R.P.
Biol. Chem. 269, 23318-23327, 1994
A;Title: The P-selectin glycoprotein ligand from human neutrophils displays sialylated, A;Reference number: A54711; MUID:94365038; PMID:7521878

A;Molecule type: protein A;Residues: 350-355;390-391,'K',393-396 <MOO> A; Gene: GDB: SELPLG

A; Cross-references: GDB:273698; OMIM:600738

A Map position: 12q24-12q24

A; Introns: #status absent

C; Keywords: disulfide bond; glycoprotein; polymorphism; tandem repeat; transmembrane pro
C; Keywords: disulfide bond; glycoprotein; polymorphism; tandem repeat; transmembrane pro
F; 1-412/Product: P-selectin glycoprotein ligand PSGL-1 precursor, short splice F; F; 1-134,145-412/Product: P-selectin glycoprotein ligand PSGL-1 precursor, short splice F; F; 1-13/Pomain: signal sequence #status predicted <SIG>F; 1-19/Pomain: extracellular #status predicted <SIG>F; 1-261/Region: 10-residue repeats (A-T/M-B-A-Q-T-T-X-P/L-A/T)
F; 117-261/Region: transmembrane #status predicted <TWM>

Gaps 10; Length 412; Indels 99.3%; Score 2015; DB 2; 97.6%; Pred. No. 2.1e-119; iive 0; Mismatches 0; Conservative Similarity 402; Query Match Matches

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C;Genetics:
A;Note: ORF71
C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein homo
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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AATEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAATEAQTTQPTGLEAQTTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 ATTTAATTTAATTTAATTTTAATTTTAATTTAATTSSATTAATTTAATTTAA
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                                                            Rikitisawa, R.; Kobayashi, T.; Kawakami, Y.; Iwai, H. J. Equine Sci. 7, 79-87, 1996
J. Equine Sci. 7, 79-87, 1996
A; Title: Nucleotide sequences of open reading frames 1, 24
A; Reference number: 222973
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-867 < KIR>
A; Residues: 1-867 < KIR>
A; Cross-references: EMBL:D88734; PIDN:BAA20038.1
A; Experimental source: isolate 3F clone; strain BK343
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 TTDTTTPSE-----ATTATTSPESTTVSASTTSA----
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                                       Accession: T45463
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       EMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTDSAAME 120
                                                                                                                                           IQTTQPAA-----TEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAATE 170
                                                                                                                                                                                                                                                                                  AQTTQPTGLEAQTTAPAAMEAQTTAPAAMEAQTTPPAAMEAQTTQTTAMEAQTTAPEATE 230
                                                                                                                                                                                                                                                                                                                                                                                                                      AQTTQPTATEAQTTPLAAMEALSTEPSATEALSMEPTTKRGLFIPFSVSSVTHKGIPMAA 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  salivary glue protein sgs-3 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 16-Jul-1999
                                                 EMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTDSAAME
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Best Local Similarity 30.8%; Pred. No. 3.2e-11;
Matches 69; Conservative 32; Mismatches 112;
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392

186 277

Gaps

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Length 867;

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----TTTAFTTESHTSP

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24 and 71 of an attenuated equin
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C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein homo
F;558-866/Domain: equine herpesvirus 1 glycoprotein homology <EHG>
                                                                                                                                                                                                                                                                                                                                                                                                                membrane glycoprotein [imported] - equine herpesvirus 1
C;Species: equine herpesvirus 1
C;Species: equine herpesvirus 1
C;Species: al-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jun-2000
C;Accession: T45462
R;Kirisawa, R; Kobayashi, T.; Kawakami, Y.; Iwai, H.
J. Equine Sci. 7, 79-87, 1996
A;Title: Nucleotide sequences of open reading frames 1, 24 and 71 of an attenuat.
A;Reference number: 222973
A;Accession: T45462
A;Accession: T4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trirprstrrrarrivprrastrrdrrraarrraarrraa----rrraarrraarrra
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| ::|| ::|| DSSTGSTSTAEPSSTFTLIPS-TAIPSTDQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
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membrane glycoprotein [imported] - equine herpesvirus 1 C;Species: equine herpesvirus 1

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55 PETEPPEMLRNSTDTTPLTGPGT--PESTTVEPAARRSTGLDAGGAVTELTTELANMGNL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 ETTTTTPTASTTTPTTTTAAPTTAATTTAVTTAASTSABTTTTATATSTPTTTTPTSTT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LAATEAQTTPPAATEAQTTQPTGLEAQTTAPAAMEAQTTAPAAMEAQTTP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAAMEAQTTOTTAMEAQTTAPEATEAQTTQPTATEAQTTPLAAMEALSTE-PSATEALSM 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPTTKRGLFIPFSVSSVTHKGIPMAA---SNLSVNYPVGAP--DHISVKQCLLAILLAL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 TPTS-----TSTSAAATTSTPTPTSAATSAESTTEAPTSTPTTPTTPSE-----AT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VATIFFVCTVVLAVRLSRKGHMYPVRNYSPTEMVCISSLLPDGGEGPSATANGGLSKAKS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TTTAFTTESHTSPDSSTGSTSTAEPSSTFTLT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-801 <KIR>
A;Residues: 1-801 <KIR>
A;Crossereferences: EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1
A;Experimental source: strain Bristol N2; clone ZK84
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZK84.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Taenor-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T29018
R;Kirsten, J.
submitted to the EMBL Data Library, April 1995
A;Reference number: Z20553
A;Reference number: Z20553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 STDSAAMEIQTTQP-----AATEAQTTPLAATEAQTTRLTATEAQ----TTP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches 169; Indels
A;Description: The DNA sequence of equine herpesvirus-1. A;Reference number: A36805 A;Accession: H36802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 250.5; DB 1
Pred. No. 2.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%;
28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 TATTSPESTTVSASTTSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGLTPEPREDR 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS-TATPSTDO 393
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R; Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
C; Gen. Virol. 79, 1197-1203, 1998
A; Title: The DNA sequence of equine herpesvirus-4.
A; Reference number: Z22173; MUD:98264497; PMID:9603335
A; Accession: T42614
A; Accession: T42614
A; Accession: T42614
A; Accession: T50 < TEL>
A; Accession: T50 < TEL>
A; Cross references: EMBL:AF030027; NID:g2605950; PIDN:AAC59591.1; PID:g2606019
A; Cross references: Exain NS80567
C; Genetics:
A; Note: 71
C; Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein home
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                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                   302
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                                                                                                                                                                                                                                                                                                                                  ----TTTAFTTESHTSP 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEPPEMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTDS 116
                                                                    217 ATTTAATTTAATTTAATTTAATTAATTSSATTAATTTAATTTAATTTAATTTAATTTAA
                                                                                                                                                       68 TOTP----STSOTPTISSSTVSTTTTSNSTNESSTATATSTATPTSTEAST--STTTST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AAMEIQTTQPAATEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAATEAQTTQP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SVSESPTSTTATTAATTTTESTTTESTTAATTTTAATTTTAATTTAATTTTAATTTTAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p)
C;Species: equine herpesvirus 1
C;Species: equine herpesvirus 1
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C;Accession: H3680;
C;Accession: H3680;
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Submitted to GenBank, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                247 AAMEALSTE-PSATEALSMEPTTKRGLFIPFSVSSVTHKGIPMAA---SNLSVNYPVGAP
                                                                                                                                                                                                                                                                                         --DHISVKQCLLAILILALVATIFFVCTVVLAVRLSRKGHMYPVRNYSPTEMVCISSLLP
                             <u>AATEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAATEAQTTQPTGLEAQTTAP</u>
                                                                                                               187 AAMEAQTTAPAAMEAQTTPPAAMEAQTTQTTAMEAQTTAPEATEAQTTQPTATEAQTTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATEAOT --- TPLAAMEALSTEPSATEALSMEPTT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTAATTTAATTTAATPTESSEASSTLAATTADTT 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 256; DB 2; 35.8%; Pred. No. 9.7e-09;
                                                                                                                                                                                                                                                                                                                               392 TIDITIPSE-----ATTAITSPESTIVSASTISA-
                                                                                                                                                                                                                                                                                                                                                                             DGGEGPSATANGGLSKAKSPGLTPEPREDR 390
                                                                                                                                                                                                                                                                                                                                                                                                        | | ::|| | ::||
DSSTGSTSTAEPSSTFTLTPS-TATPSTDQ 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 35.8%
Matches 77; Conservative
                                                                                                                                                                                                                                                                                         303
                           127
                                                                                                                                                                                                                                                                                                                                                                          361
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VGBEX1
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816

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high molecular mass nuclear antigen - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18535
R;Shimada, K.; Harata, M.; Mizuno, S.
C;Accession: T18535
R;Shimada, K.; Harata, M.; Mizuno, S.
A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick, A;Reference number: Z18955; MUID:9803440; PMID:9365273
A;Accession: T18535
A;Accession: T18535
A;Accession: Drellinary; translated from GB/EMBL/DDBJ
A;Accession: L1151 cRHI>
A;Residues: 1-1151 cRHI>
A;Cross-references: EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 PEATEAQTTQPTATEAQTTPLAAMEALST-----EPSATEALSMEPTTKRGLFIPFSV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           889 QSPPMGATTTQSPPMGASTPQAPPTVAGSPTPPPPIPPSPTAQTSPQPMSKSPPPDPPKA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-770 <WIL>
A;Cross-references: EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F56H9.1
A;Experimental source: clone F56H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F56H9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 GLEAQTT-----APAAMEAQTTAPAAMEA-QTTPPAAMEAQTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     829 PMGAATTLMSPMGAATTPQPSPMGAVTTQPPPMAATNTTQPPPMAASTPQSTPMGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ---PAATEAQTTPLAATEAQTTRLTATEA----QTTPL-AATEAQTTPPAATEAQTTQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 IDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTDSAAMEIQTTQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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A;Map position: 5
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
10.1%; Score 205.5; DB 2; 29.8%; Pred. No. 2.3e-05; tive 31; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.1%; Score 204.5; DB 2;
Best Local Similarity 27.0%; Pred. No. 1.7e-05;
Matches 81; Conservative 28; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | | : | : | 949 PSAAAAQTSPAAHVANASPGVTAVSPAPIGVTE 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 SSVTHKGIPMA-ASNLSVNYPVGAPDHISVKQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Burton, J.
submitted to the EMBL Data Library, June 1996
Reference number: 219618
A;Accession: T22808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 81; Conserva
                                                                               320 VATIFF 325
                                                                                                              | |:||
817 VLTMFF 822
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                        A;Map position: 2
A;Introns: 22/2; 45/3; 108/1
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Map position: X
;Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1
;Superfamily: Epstein-Barr virus membrane antigen gp350
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| PIEAPAT-DAATLETAPAPAABPAAAGYDAPSSVPEBTPAPAAD-ETPAPAPA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Residues: 1-825 <NHA>;
;Cross-references: EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP:C12D12.1
;Experimental source: strain Bristol N2; clone C12D12
                                                                                                                                                                                                                                         71 PLTGPGTPESTTVE-----PAARRSTGLDAGGAVTELTTELANMGNLSTDSAAME 120
                                                                                                                                                                                                                                                                                                                                                                                      689 ETPAPAPAEETPASAPAAEETPAPAPAAEEAPAPAAPETPAPAAEGAAAPAIVSSG 748
                                                                                                                                                                                                                                                                                                                                               121 IOTTOPAATEAOTTPLAATEAOTTRLTATEAOTTPLAATEAOTTP-----PA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 ATEAQTTOPTGLEAQTTAPAAMEAQTTAPAAME----AQTTPPAAMEAQTTQTTAMEAQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         629 VEETPAPAPAVEETPAPAPAAEETPAPAAAEYAAPVAEETPAPAAEETPAPAQAAE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 TT---APEATEAQTTQPTATEAQTTPLAAMEALSTEPSATE-----ALSMEPTTKRG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 PITIKPVVITNSVIPSIGITIVPVPITIGSPITĮQITAPVIKPIVPSSITĮQIAPPVITPIS 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTPLAA----TEAQTTPPAATEAQTTQPTGLEAQTTAPAAMEAQTTAPAAMEAQTTPPPAA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C12D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T29634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 MEAQTIQTIAMEAQTIAPEATEA--QTTQPTATEAQTIPLAAMEALSTEPSATEALSMEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 PETEPPEMLRNS-----VEPAARRSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 LDAGGAVTELTTELANMGNLSTDSAAMEIQTTQPAATEAQTTPLAATEAQTTRLTATEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TAPTVPPVTTTTTTTTTTTTTTTTTTTTTTT
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                                                                                                                                    Length 801;
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R;Nhan, M; Hawkins, J.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C12D12.
A;Reference number: Z20656
A;Accession: T29634
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:U51998; PIDN:AAA956080.1; GSPDB:GNO(A;Experimental source: strain Bristol N2; clone C12D12
C;Genetics: C.
                                                                                                                              Query Match 11.2%; Score 226.5; DB 2; Best Local Similarity 30.6%; Pred. No. 7.4e-07; Matches 82; Conservative 22; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.4%; Score 210.5; DB 2; Best Local Similarity 27.5%; Pred. No. 7.7e-06; Matches 84; Conservative 23; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 YDAAQSTDTVVASSAPATSSDASGATNY 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 LFIPFSVSSVTHKGIPMAASNLS--VNY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: CESP:C12D12.1
  A; Gene: CESP: ZK84.1
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A;Molecule type: DNA
A;Residues: 1-161 <SCA>
A;Cresidues: 1-161 <SCA>
A;Cresidues: 1-161 <SCA>
C;Genetics:
A;Gene: SGD:DAN4; MIPS:YJR151c
                                                                                                                                                                                                                                                                                                                                   antifreeze glycopeptide AFGP polyprotein precursor [imported] - Boreogadus saida C;Species: Boreogadus saida C;Species: 21-dan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T44768 A.L.; Cheng, C.H.C. Proc. Natl. Acad. Sci. U.S.A. 94, 3817-3822, 1997 A;Title: Convergent evolution of antifreeze glycopeptides in Antarctic notothenioid A;Reference number: Z22834; MUID:97268653; PMID:9108061
                                                          3038 QESIASSTSEVIILPIDSTTFLIPPPSTTTELIYTVSSDGTLEPITS-APT-----T 3089
                           KQCLLA----ILILALVATIFFV----CTVVLAVRLSRKGHMYPVRNYSPTEMVCISSL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    РАКААКААТРАТАТГАТААТРАТРАТРАТААТОАТААТААТРАКААТРАТРАТРАТРАТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTTRLTATEAQTTPLAATBAQTTPPAATEAQTTQPTGLEAQTTAPAAMEAQTTAPAAMEA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 PATAATAATAATAATAATPARAARAATPATAATPATAATAATAATAATAATAATAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTTPPAAMEAOT--TOTTAMEAQTTAPEATEAQTTQPTATEAQTTPLAAMEALSTEPSAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EA-----LSMEPTTKRGLFIPFSVSSVTHKGIPMA--ASNLSVNYPVGAPDHISVKQC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 AATAATAATAATAPTPARAARAATPATGATPATAPTAGTAATAATAATAATPARASTPAT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U43200; NID:g2078482; PIDN:AAC60129.1; PID:g2078483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YJR151c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J2223; serine/threonine-rich protein YJR151c
C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C;Accession: S57180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 VEPAARRSTGLDAGGAVTELTTEL-ANMGNLSTDSAAMEIQTTQPAATEAQTTPLAATEA
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ubulited to the Protein Sequence Database, September 1995
A;Reference number: S57169
A;Accession: S57180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Score 194.5; DB 2; 27.7%; Pred. No. 4.5e-05; iive 14; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-507 <CHE>
                                                                                                                                                                                                       3090 IGSSSEGPTTATSTEPIYTASPDTSPE 3116
                                                                                                                                                LPDGGEGPSATANGGLSKAKSPGLTPE 385
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Matches 87; Conserv
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A;Introns: 18/1; 73/2; 101/3; 241/2; 251/1; 327/3; 383/3; 455/3; 494/1; 793/1; 905/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2819 QTVSETDGTTSMFQTSEPSTWQTSNEPTSEPTTVPLETSTWQNT--DGTSMEPTSVTPEE 2876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2877 GOTTSPTATTLIFVDST-LETVTTT----EATTISEGTISQE-----DFGTTSMTTSE 2924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2925 SEGTSPEYITSEATLEPITSTVESTTTIMISTISELISTSDYTTQSSDSTSMEP----- 2978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2979 -IMSSTSTFESSAFPTPDGFTLEPITTTMTTEYPDGTTMTSPDATLPILTTTSSEYYTST 3037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 FIPFSVSSVTHKGIPM-----AASNLSVNYPVG----APD------HISV 307
TEPPEMLRNSTDTTPLTGPGT-PESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTD 115
                                                                                                                    SAAMBIQTTQPAATBAQTTPLAATBAQTTRLTATBAQTTPLAATBAQTTPPAATBAQTT- 174
                                                                                                                                                                      131 TVPPTTTSSTTT-----TTVPPTTTSTTTTVPPTTTSTTTTTTVPATTTSTTT 182
                                                                                                                                                                                                                                                                                                                                                        TAPEATEAQTT---QPTATEAQTTPLAAMEALSTEPSATEALSMEPTTKRGLFIPF-SVS 279
                                                                                                                                                                                                                                                                                                                                                                                                               183 TVPPTTSTTTTTTVPPTTTTT--TTVPPTTTSSTTTTTTTTTPTTTTTMMIPICSLD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 SVTH-KG-----IPMAASNLSVNYPVGAPDHISVKQCLLAILILALVATIFFVCTVV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ::|: || :
-----MQSLSTMQISCTAI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-3191 <WIL>
A; Residues: 1-3191 <WIL>
A; Cross-references: EMBL: Z81094; PIDN: CAB03155.1; GSPDB: GN00023; CESP: T01D3.1
A; Experimental source: clone F58G11
R; Steward, C.
Submitted to the EMBL Data Library, October 1996
A; Reference number: Z19870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-3191 < W12>
A; Cross-references: EMBL: Z81110; PIDN: CAB03261.1; GSPDB: GN00023; CESP: T01D3.1
A; Experimental source: clone T01D3
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T01D3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T22945; T24295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 AQTIPPAATEAQTIQPIGLEAQTIAPAAMEAQTIAPAAMEAQTIPPAAMEAQTIQTIAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 AQTTAPE-ATEAQTTQP-TATEAQTTPL---AAMEALSTEPSAT---EALSMEPTTKRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 MGNLSTDSAAMEIQTTQPA-----ATEAQTTPLAATEAQTTRLTATEAQTTPLAATE
                                                       TVVPITTTSSSSTTSSTTTTTVPVSTTTSSTTTT-----TVPSTTTSSATTTTVPST
                                                                                                                                                                                                                                         ---PPAAMEAQTT----QTTAMEAQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1996
A;Reference number: Z19640
A;Accession: T22945
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: T24295
Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SLTFGKGDNFQPQVDIDVTYSNLVANIIPGTMD----
                                                                                                                                                                                                                                      -- OPTGLEAQTTAPAAMEAQTTAPAAMEAQTT-
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C, Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C, Accession: T21460
R;Wilkinson, J.
Submitted to the EMBL Data Library, March 1995
A, Reference number: 219425
A, Reference number: 219426
A, Status: preliminary, translated from GB/EMBL/DDBJ
A, Status: preliminary, translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-796 < WIL>
A, Molecule type: DNA
A, Residues: L796 < WIL>
A, Gross-references: EMBL: 248582; PIDN: CAA88469.1; GSPDB: GN00020; CESP: ZK945.10
A, Experimental source: clone F27E5
C, Genetics:
C, Genetics:
A, Gene: CESP: ZK945.10
A, Map position: 2
A, Introns: 62/3; 124/3; 169/1; 216/1; 262/3; 371/1; 581/3; 608/1
                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                 101 ELTTELANMGNLSTDSAAMEIQTTQPAATEAQTTPLAATEAQTTRLTATEAQTTPLAATE 160
                                                                                                                                                                                                                                                                                                                                                                     120 AIPT---STSTTTTKSSTSTTPTTTTTSTTSTTSTTSTTSTTPTTSTTSTTSTTPTTFT-175
                                                                                                                                                                                                                                                                                                                                                                                                                        161 AQTTPPAATEA-----QTTQPTGLEAQTTAPAAMEAQTTAPAAMEAQTTPPAAMEAQTTQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 ISTIPITSTISTIPITSTISTIPITSTISTISTISTISTISTISTISTISTISTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 TTAMEAQTTAPEATEAQTTQPTATEAQTTPLAA----MEALSTEP-----SATEALS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 TTPTTSTTSTTSQTSTKSTTPTTSSTSTTPTTSTTSTAPTTSTTSTTSTTSTTSTTSTTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 NSTDTT---PLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGN-----LSTD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 SAAMEIQTTQ--PAATEAQTTPLAATEAQTT--RLTATEAQTTPLAATEAQTTPPAATEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 OTTOPTGLEAQTTAPAAMEAQT--TAPAAMEAQTTPPAAMEAQTTQTTAMEAQTTAPEAT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 EAQTTOPTATEAQTTPLAAMEALSTEPSATEALSMEPTTKRGLF1PF-SVSSVTHKG1PM 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ZK945.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21460
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                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 AASNLSVNYPVGAPDHISVKQCLLAILILALVATIFFVCTVVLAVRLSRKGHMYP----
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                                                                                                      Length 1161;
                                                                                                      Query Match 9.6%; Score 194; DB 2; Length 11 Best Local Similarity 26.6%; Pred. No. 0.00012; Matches 73; Conservative 30; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 TAPTTST-TSSTFSTSSASSVISTTATTSTFF 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 MEPITKRGLFIPFSVSSVTHKGIPMAASNLSVNY 297
                                                                                                                                                                                                                ETEPPEMLRNSTD----TTPLTG-
A;Cross-references: SGD:S0003912
A;Map position: 10R
C;Keywords: transmembrane protein
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Best Local S:
Matches 87
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hypothetical threonine/asparagine-rich protein - fission yeast (Schizosaccharomyces pomt C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 0.3 -Dec-1999 #sext_change 08-Dec-2000 C; Accession: 741309; 740875 F. Riyood, V.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Wambutt, R.; Wedler, E. Submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL022245; NID:g4584240; PIDN:CAA18304.1; PID:g2995364; GSPDB:GR
A;Experimental source: strain 972h-; cosmid c320
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Mesidues: 468-658 e/MOO2>
A; Mesidues: 468-658 e/MOO2
A; Cross-references: EMBL; AL031764; NID: 93668147; PIDN: CAA21105.1; PID: 93668148; GSPDB: GNA; Experimental source: strain 972h-; cosmid c1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                677
  VRNYSPTEMVCISSLLPDGGEGPSATANGGLSKA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 TTPMEEI--TTITTPMEETTTITPMVETTTILPMAAMTTPMVETTTIPTVETTTPMVET 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 PAATEAQTTQPTGLEAQTTAPAAMEAQTTAPAAMEAQTTPPAAMEAQTTQTTAMEAQTTA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-----EATEAQTTQPT----ATEAQTTPLAAMEALSTE----PSATEALSMEP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- TSAVASSTSSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 TEPPEMLRNSTDTTPL--TGPGTP--ESTTVEPAARRSTGLDAGGAVTELTTELANMGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 STDSAAMEIQTTQPAA-----TEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 MVET---TTIPT-VETMTT--PMVEAMTILP--MAAMTTP-----MEETTTTPMEETTTT
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9.5%; Score 193; DB 2; Length 658
Best Local Similarity 29.6%; Pred. No. 7.5e-05;
Matches 87; Conservative 33; Mismatches 114; Indels
                                  KSPGLT-----PEPREDREGDDLT 396
                                                                                                                                                      STPSSTLSTSTVTEPSSTRSSDSTT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: SPDB:SPCC320.02c; SPDB:SPCC1235.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-658 <WOOl>
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z21986
A; Accession: T41309
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A;Accession: T40875
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Maximum DB
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Maximum Match 100%
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   925.5

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196.5

197.5

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## ALIGNMENTS

RESULHYAN  SEPL_HHMAN  CO 14373; O12775;  DT 01-MOV-1997 [Ral. 35, Created) DT 01-MOV-1997 [Ral. 35, Created) DT 01-MOV-1997 [Ral. 36, Last sequence update) DT 01-MOV-1997 [Ral. 36, Last sequence update) DT 16-OCT-2001 [Ral. 40, Last sequence update) DT 16-OCT
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                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATABASE: NAME=PROW; NOTE=CD guide CD162 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd162.htm".
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an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                 EMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTDSAAME
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-I- FUNCTION: BINDS TO P-, E- AND L-SELECTINS. THE CALCIUM-DEPENDENT HIGH AFFINITY INTERACTION WITH P-SELECTIN MEDIATES THE TETHERING AND ROLLING OF NEUTROPHILS AND T-LYMPHOCYTES ON ENDOTHELIAL CELLS.
-I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- PTM: HEAVILY O-GLYCOSYLATED, ALSO N-GLYCOSYLATED (BY SIMILARITY).
-I- PTM: HEAVILY O-GLYCOSYLATED, ALSO N-GLYCOSYLATED (BY SIMILARITY).
-I- PTM: HEAVILY O-GLYCOSYLATED, ALSO N-GLYCOSYLATED (BY SIMILARITY).
                                                                                                                                                                                                                CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=96220265; PubMed=8639776;
Yang J., Galipeau J., Kozak C., Furie B.C., Furie B.;
"Mouse P-selectin glycoprotein ligand 1: molecular cloning,
chromosomal localization, and expression of a functional P-selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
P-selectin glycoprotein ligand 1 precursor (PSGL-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                Sulfation
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                               PROPEP
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  Chordata;
Rodentia;
                                                                                                              POTENTIAL.

BY SIMILARITY.

P-SELECTIN GLYCOPROTEIN LIGAND 1

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

SULFATION (POTENTIAL).

SULFATION (POTENTIAL).
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
10 X 10 AA TANDEM REPEAT
1.
2.
                                                                                                                                                                                                                                                                                                                                    Transmembrane;
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                                              TANDEM REPEATS
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                                                                       (POTENTIAL)
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DT 16---
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GN 8G8
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Best Local S
Matches 194
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STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A.,
                                                                                                                                                                                                                                                                                                                                                                           P02840; Q9VTJ2;
21-UTL-1986 (Rel. 01, Last sequence update)
21-UTL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Salivary glue protein Sgs-3 precursor.
SGS3 OR CG11720.
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrusta
Insecta; Pterygota; Neoptera; Endopterygota; Diptera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                    Garfinkel M.D., Pruitt R.E., Meyerow "DNA sequences, gene regulation and Drosophila 68C glue gene Cluster."; J. Mol. Biol. 168:765-789(1983).
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                        MEDLINE=83294545; PubMed=6411930;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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               Gocayne J.D.
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Harndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harndon R.C., Basu A., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Hortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.J.,
RA Kimmel B.E., Kodita C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodita C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Woy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Kinska R., Tector C., Turner R., Venter E., Wang X.,
RA Yella, Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Yella, Wang S.A., Woodage T., Worley K.C., Shan M., Zhang G., Zhao Q.A., Zheng L.,
RA Hostin M., Wars E. W., Zhong W., Zhan M., Smith H.O.,
RA Holland R.G., Shong M., Shan M., Shan S., Zhu X., Smith H.O.,
RA H
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Development 118:613-627(1993).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martin C.H., Mayeda C.A., Meyerowitz E. "Evolution and expression of the Sgs-3 J. Mol. Biol. 201:273-287(1988).
                                                                                                                                                                                                                                                                                                         between
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                                                                                                                                                                                                                                                                                                                                         SIDEMENT 118:613-64/11757;
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICTY: SALIVARY GLAND SPECIFIC.
DEVELOPMENTAL STAGE: IN THE SALIVARY GLANDS OF MID INSTAR LARVAE LEVELS DRAWATICALLY INCREASE DURING PUFF STAGE 1 AT 98-106 HOURS
OF DEVELOPMENT. LEVELS REMAIN CONSTANT AND ABUNDANT IN LATE LARVAE
OF DEVELOPMENT. LEVELS REMAIN CONSTANT AND ABUNDANT IN LATE LARVAE
OF DEVELOPMENT. LEVELS REMAIN CONSTANT AND ABUNDANT IN LATE LARVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=8223281;
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EMBL; X01918; CAA25994.1; EMBL; AE003544; AAF50056: EMBL; X78392; CAA55154.1;

CAA25994.1; -.

AAF50056.1;

FlyBase;

FBgn0003373; Sgs3

Signal.

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POTENTIAL. SALIVARY GLUE

PROTEIN

PIR; A03329; GSFF3

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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92295566; PubMed=1318606;
Telford E.A.R., Watson M.S., McBride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein
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                                                                                                                                                                                                                                                         PIR; H36802;
                                                                                                                                                                                                                                                                   EMBL; M86664; AAB02506.1;
                                                                                                                                                                                                                                                                                                                                                                                          "The DNA sequence of equine herpesvirus-1."; Virology 189:304-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=31520;
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                  ETTTTTPTASTTTPTTTTAAPTTAATTTAVTTAASTSAETTTATATATSTPTTTTPTSTT
                                        STDSAAMEIQTTQP-----
                                                                                      PETEPPEMLRNSTDTTPLTGPGT--PESTTVEPAARRSTGLDAGGAVTELTTELANMGNL
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                                                                   PTTSPP-
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Pred. No. 4.3e
33; Mismatches
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POTENTIAL.
GLYCOPROTEIN X
SER/THR-RICH.
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Pred. No. 8.
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           AGENTS AT MUCOSAL SURFACES.

-!- SUBUNIT: MULTIMERIC.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: COLON, SWALL INTESTINE, COLONIC TU
BRONCHUS, CERVIX AND GALL BLADDER.
-!- PIM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
-!- POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORP
VARIES AMONG DIFFERENT ALLELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                        and polymorphism.";
J. Clin. Invest. 88:1005-1013(1991)
-!- FUNCTION: COATS THE EPITHELIA O
                                                                                                                                                                                                                                                                                                                                                 Gum J.
Kim Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gum J.R. Jr., Hicks J.W., Toribara N.W., "Molecular cloning of human intestinal mu Identification of the amino terminus and to prepro-von Willebrand factor."; 1. Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN 1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat Mucin 2 precursor (Intestinal mucin 2).
                                                                                                                                                                                                                                                                                                                    both
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mucin 2 precursor MUC2 OR SMUC.
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Q02817; Q14878;
                                                                                                                                                                                                                               Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Petersen G.M., Kim Y.S.;
                                                                                                                                                                                                                                                                                                        J. Biol.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93016075; PubMed=1400449;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 626-1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94132002; PubMed=8300571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                  "MUC-2 human small
                                                                                                                                                                                                                                                            MEDLINE=91358717; PubMed=1885763
                                                                                                                                                                                                                                                                         SEQUENCE OF 1343-1895 AND 4176-4195 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                             OTHER MUCUS MEMBRANE-CONTAINING PROTECTIVE, LUBRICATING BARRIER
 SIMILARITY:
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N4 precursor.
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Pred. No. 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complex array of regulatory sites.";
Nucleic Acids Res. 29:799-808(2001).
-!- FUNCTION: COMPONENT OF THE CELL WALL (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21113168; PubMed=11160904; Cohen B.D., Sertil O., Abramova N.E., Davies K.J., Lowry C.V. Miduction and repression of DAVI and the family of anaerobic mannoprotein genes in Saccharomyces cerevisiae occurs through
                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR000992; SRP1_TIP1.
Pfam; PP00660; SRP1_TIP1; 1.
PROSITE; PS00724; SRP1_TIP1; 1.
Cell_wall; Glycoprotein; Membrane; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license or send an email to license@
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                               Similarity 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
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                                                                             TAPTTST-TSSTFSTSSASASSVISTTATTSTTF
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llarity 26.6%;
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Pred. No. 0.00015;
D; Mismatches 125;
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CELL WALL PROTEIN DAN4.
REMOVED IN WATURE FORM (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a copyred threen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Durbin R.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ-i- SUBCELL/LAR LOCATION: Integral membrane pi-i- SIMILARITY: CONTAINS 1 GPS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein ZK945.9 in chromosome II
ZK945.9/ZK945.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical DOMAIN
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SMART; SM00308; LH2; 1
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Pfam; PF01477; PLAT; 1. 
Pfam; PF01825; GPS; 1.
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InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR000636; M+channel_nlg.
InterPro; IPR000203; PKD_cys_rIch.
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                                                                                                                                                                                                                                            SEQUENCE
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NCBI_TaxID=6239;
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                                  389
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                                                                                                                          65 NSTDTT---PLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGN-----LSTD
                                                                                                                                                                       87;
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QTTQPTGLEAQTTAPAAMEAQT--TAPAAMEAQTTPPAAMEAQTTQTTAMEAQTTAPEAT
                                  TTSTTFTTTMLTSTTTEEPSTSTTTTEVTSTSSTVTTTEPTTTLTTSTASTSTTEPSTST
                                                                SAAMEIQTTQ--PAATEAQTTPLAATEAQTT--RLTATEAQTTPLAATEAQTTPPAATEA
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(FEB-1995)
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Caenorhabditis.
                                                                                                                                                                       57;
                                                                                                                                                                                         Score 193.5;
Pred. No. 0.0
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  (See http://www.isb-sib.ch/announce/
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MEDLINE-89031230; PubMed=3141213;
Pardo J.M., Ianez E., Zalacain M., Claros
"Similar short elements in the 5' regions
from Saccharomyces cerevisiae.";
PEBS Lett. 239:179-184(1988)
-!- CATALYTIC ACTIVITY: Hydrolysis of ter
glucose residues successively from no
with release of beta-D-glucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P08640; P08068;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan glucosidase) (1,4-alpha-D-glucan glucohydrolase).
STA1 OR STA2 OR MALS OR YIR019C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Whitehead S.;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-242 AND 762-1331 FROM MEDLINE=87194600; PubMed=3106330;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
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STRAIN=SPX101-1C;
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SIMILARITY: TO S.POMBE SPBC215.13.
SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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EMBL; M16164; AAA35012.1; -
EMBL; M16165; AAA35015.1; -
EMBL; X13857; CAA32069.1; -
PIR; B26877; B26877.
PIR; A26877; B26877.
PIR; S48478; S48478.
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SEQUENCE
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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15-JUN-2002 (Rel.
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01-OCT-1994 (Rel.
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SIGNAL 1 21
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01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Integumentary mucin C.1 (FIM-C.1) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kenopodinae;
                                                                                                             BIOL Chem. 267:24620-24624(1992).

BIOL Chem. 267:24620-24624(1992).

FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL INFECTIONS. PROTECTS THE EPITHELIA FROM EXTERNAL ENVIRONMEN.

SUBCELLULAR LOCATION: Secreted.

ALTERNATIVE PRODUCTS: At least 7 isoforms; 1 (shown here),

4, 5, 6 and 7; may be produced by alternative splicing.

TISSUE SEBCIFICITY: SKIN.

PIM: EXTENSIVELY O-GLYCOSYLATED.

SIMILARITY: CONTAINS 6 P-TYPE (TREFOIL) DOMAINS.
s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation Buropean Bloinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no wa
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                                                               MEDLINE-90316191; PubMed=2196180;
Hauser F., Gertzen E.M., Hoffmann W.;
"Expression of spasmolysin (FIM-A.1): an integumentary
Yenopus laevis.";
Exp. Cell Res. 189:157-162(1990).
-i- FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICH
INFECTIONS. PROTECTS THE EPITHELIA FROM EXTERNAL EN
-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: EXPRESSED AND STORED EXCLUSIVED
MUCOUS GLANDS OF THE SKIN.
-i- PTM: EXTENSIVELY O-GLYCOSYLATED. CONSIST OF ABOUT .
AND 30% PROTEIN.
-i- SIMILARITY: CONTAINS 4 P-TYPE (TREFOIL) DOMAINS.
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                                                                                                                                                                                                                                                                        "A new repetitive protein from Xenopus 1 to pancreatic spasmolytic polypeptide."; J. Biol. Chem. 263:7686-7690(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Integumentary mucin A.1 precursor (FIM-A.1) (
Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XENLA
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                                                                                                                                                                                                                                                                                                                 Hoffmann W.;
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            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation -
European Bioinformatics Institute. There are no restrictions on its
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PROSITE; PS00025; 1
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                                 Drosophila erecta (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Braci
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF00088; trefoil; 4.
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P13290;
01-JAN-1990
01-JAN-1990
01-NOV-1997
                                                    Dolan A.;
Submitted
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-87111457; PubMed=3027242;
MCGeoch D.J., Moss H.W.M., McNab D., Frame M.C.;
"DNA sequence and genetic content of the HindIII 1 r
"DNA sequence component of the herpes simplex virus t
short unique component of the encoding glycoprotein G,
                                                                                                                                                                                                  Viruses; dsDNA viruses,
Alphaherpesvirinae; Sim,
NCBI_TaxID=10315;
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J. Mol. Bio
                                                                                                  comparisons.";
J. Gen. Virol.
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          - MISCELLANEOUS:
2: GH, GB, GC,
- MISCELLANEOUS:
HSV-1.
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HERE ARE SEVEN EXTERNAL GLYCOPROTEINS
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MEDLINE=96144270; PubMed=8566773;
Pishko E.J., Kirkland T.N., Cole G.T.;
Pishko E.J., Kirkland T.N., Cole G.T.;
"Isolation and characterization of two chitinase-encoding
"Isolation and characterization of chitinase-encoding
(cts1,_cts2) from the fungus Coccidioides immitis.";
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HSSP; P23472; 2HVM.
InterPro; IPR001579; Chitinase 18/2.
InterPro; IPR001273; Glyco_hydro_18; 1.
PR001704; Glyco_hydro_18; 1.
PROSITE; PS01095; CHTTINASE_18; 1.
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SIGNAL
            Eukaryota;
                        Mus musculus (Mouse)
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                                                                                                                                                                                        YPVGAPDHI
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                                              precursor.
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 Chordata;
Rodentia;
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                                                         sequence update) annotation updat
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Pred. No. 0.0
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ENDOCHITINASE 2.
N-LINKED (GLCNAC
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                          update
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Eutheria;

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Pfam; PF00629; MAM; 3.
Pfam; PF01826; TIL; 25.
Pfam; PF02345; TILa; 25.
SMART; SM00181; EGF; 2.
SMART; SM00181; EGF; 2.
SMART; SM00274; FOLN; 11.
SMART; SM00214; VWC; 17.
SMART; SM00216; VWD; 4.
SMART; SM00216; VWD; 4.
PROSITE; PS00072; EGF 1; 1.
PROSITE; PS01166; EGF 2; 1E
PROSITE; PS01166; EGF 2; 1E
PROSITE; PS00740; MAM 1; FZ
PROSITE
                                                                                                                                                                                                                                                                          InterPro; IPR000561; EGP-like.
InterPro; IPR003645; FOIN.
InterPro; IPR003698; MAM domain.
InterPro; IPR002919; TIL_Cysrich.
InterPro; IPR00328; TILa_Cysrich.
InterPro; IPR001007; VWF_C.
InterPro; IPR0011007; VWF_D.
Pfam; PP00094; Vwd; 4.
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SIGNALING:
SIGNALING:
SIGNALING:
SUBCULIVE PROBABLY FORMS COVALENT OLIGOMERS.

SUBCULIVIAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD.

TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.

DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE ZONA PELLUCIDA.

DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVLOUCTAL ISTHMUS.

DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).

SIMILARITY: CONTAINS 3 MAM DOMAINS.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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J. Biol. (
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Genomics 41:119-122(1997).
-i- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNI
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EMBL; U83190; AAC53125.1; -.
MGD; MGI:106656; Zan.
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Gao Z., Garbers D.L.;
"Species diversity in the structure
membrane protein containing multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 4864-5376 FROM N.A. TISSUE=Testis;
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TISSUE=Testis;
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Pred. No. 0.0: 4; Mismatches

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Indels

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Gaps

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ID 1-NOV
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P41809;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94156857; PubMed=8113191;
Kasahara S., Yamada H., Mio T., Shiratori Y., Miyamoto C.,
Kasahara S., Yamada H., Mio T., Shiratori Y., Miyamoto C.,
Yabe T., Nakajima T., Ichishima E., Furuichi Y.;
Yabe T., Nakajima T., Ichishima E., Furuichi Y.;
Yabe T., Nakajima T., Ichishima E., Furuichi Y.;
"Cloning of the Saccharomyces cerevisiae gene whose overexpression
overcomes the effects of HM-1 killer toxin, which inhibits
beta-glucan synthesis.";
J. Bacteriol. 176:1488-1499(1994).
J. Bacteriol. 176:1488-1499(1994).
J. Bacteriol. 176:1488-1499(1994).
-i- FUNCTION: COULD REGULATE BETA-GLUCAN SYNTHESIS. OVEREXPRESSION
PROVIDES RESISTANCE TO HM-1 KILLER TOXIN.
-i- SUBCELIULAR LOCATION: Type I membrane protein (Probable).
                                                                                                                                                                                                                                                                                                           TRANSMEM DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hansenula MRAKII killer toxin-resistant protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKR1 OR YDR420W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S an email to license@isb-sib.ch).
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Y-T-S-S-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat;
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PROTEIN 1.
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Search completed: July 14, 2003, 06:15:13 Job time : 27 secs

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Maximum Match 100%
Listing first 45 summaries
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"Nucleotide sequences of open reading
attenuated equine herpesvirus-1.";
J. Equine Sci 7:79-87(1996).
EMBL; D88734; BAA20038.1; -.
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Q8V0M3;
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O39781;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
PRINTS; PR00308; ANTIFREEZEI.

NON TER 372 372

SEQUENCE 372 AA; 34391 MW:
                                                                Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AY034637; AAK61477.1; InterPro; IPR000104; Antifreeze_1.
                                                                                                                                  STRAIN=974/91;
Huang J.-A., Ficorilli N., Hartley
Huang J.-A., Ficorilli N., Hartley
"Polymorphism of open reading frame
and EHV1.";
                                                                                                                                                                                                                                                          Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10326;
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"Nucleotide sequences of open reading
"thenuated equine herpesvirus-1.";
J. Equine Sci 7:79-87(1996).
EMBL; D88733; BAA20037.1; -.
SEQUENCE 866 AA; 86463 MW; 153BD14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Membrane glycoprotein.
Equine herpesvirus 1.
Viruses; dsDMA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
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01-JUN-2002 (TrEMBLrel. 21,
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Last sequence update)
Last annotation updat
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Pred. No. 7.2e-09;
9; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 263; DB
Pred. No. 1.6e-
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen G.P., Studdert M. f equine herpesvirus 4
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RESULT

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IQ8VOL8
AC Q8VOL9
AC Q8

                                                                                         RESULT 7
Q8V0L5
ID Q8V0
AC Q8V0
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Best Local Similarity
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Best Local Similarity
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Q8V0L5;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Q8V0L8;
01-MAR-2002
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01-MAR-2002 (TrEMBLrel. 20, Last seque
01-JUN-2002 (TrEMBLrel. 21, Last annot
Glycoprotein gp2 (Fragment).
Equine herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
                                                                                         EMBL; AY034645; AAK61485;1; -.
InterPro; IPRO00104; Antifreeze 1.
PRINTS; PRO00308; ANTIFREEZEI.
SEQUENCE 826 AA; 82915 MW; F5E
                                                                                                                                                                                                                            STRAIN=438/77;
Huang J.-A., Ficorilli N., Hartley C.A., Allen G.
                                                                                                                                                                                                                                                                                                                                         Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10326;
                                                                                                                                                                                                                                                                                                                                                                                                       Equine herpesvirus 1. Viruses; dsDNA viruses,
                                                                                                                                                                                                                  "Polymorphism of open reading frame
and EHV1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein gp2.
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PRINTS; PR00308; ANTIFREEZEI.
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                                                                                                                                                                                       Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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  Conservative
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                   12.9%; Score 261; DB 1
29.4%; Pred. No. 5e-08;
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21,
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  Mismatches
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                                                                                                                                                                                                                                                          Allen G.P., Studdert M.J.;
                                          DB 12;
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40;
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Best Local Similarity
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01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2001) to the EMBL/G
EMBL; AY034639; AAK61479.1; -.
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
NON_TER 337 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equine herpesvirus 1.
Viruses; dsDNA viruses, no RNA stac
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huang J.-A., Ficorilli N., Hartley C.A., "Polymorphism of open reading frame 71 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=1053A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein gp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VOM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CM0A8D
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                                           EAQTTAPEATEAQTTQPTATEAQTTPLAAMEALSTE-PSATEALSMEPTT
                                                                                        eaqtteaateaqttqptgleaqttaaaaaaqttapaameaqttppaameaqttqttam
                                                                                                                                                                                                                                                                          PTSTSTETTTTTPTASTTTPTTTTAAPTTAATTTAVTTAASTSAETTTATATATSTPTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 AA;
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31272 MW;
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                                                                                                                                                                                                                            ---DSAAMEIQTTOPAATEAQTTPLAATEAQTTRLTATEAQTTPLAAT
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Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                             Score 259;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7771F755727A6E1C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                       Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen G.
of equine
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herpesvirus
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330
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(EHV4)
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RESULT. Q8V0L9

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RESULT
O39307
ID
O3307
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Best Local Similarity
Matches 78; Conserv
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039307;
01-JAN-1998
01-JAN-1998
01-DEC-2001
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Q8V0L9;
01-MAR-2002
01-MAR-2002
01-JUN-2002
MEDLINE=93119267, PubMed=8380320;
Nagesha H.S., Crabb B.S., Studdert M.J.;
"Analysis of the nuclectide sequence of :
the unique short region of the equine he
                                                           SEQUENCE OF 1-111
STRAIN=NS80567;
MEDLINE=93119267;
                                                                                                                                                          MEDLINE=93389454; PubMed=8397286; Cullinane A.A., Neilan J., Wilson L., Davison "The DNA sequence of the equine herpesvirus 4 glycoprotein gpl7/18, the homologue of herpes glycoprotein gp.";
                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=1074/94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein gp2 (Fragment)
Equine herpesvirus 1.
                                                                                                                                                                                                                                                                                            SEQUENCE OF 685-750
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10331;
                                                                                                                                                                                                                                                                                                                                                                                           Equine herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      G (TrEMBLrel. 05, Created)

HTEMBLrel. 05, Last sequence update)

Last annotation update)

counterpart of HSV-1 gene US5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
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                                                                                                                                             74:1959-1964(1993)
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                                                                                                      FROM N.
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21,
                                                                                                                                                                                                                                                                                          N.A.
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Last sequence update)
Last annotation updat
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Pred.
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No. 3.6
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e 71 of
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  herpesvirus
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                       five
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of equine
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                     genes
                                                                                                                                                                                   A.J., Allen G.
gene encoding
simplex virus
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01-MAR-2002
01-MAR-2002
01-JUN-2002
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                                                                                                                                      Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
EMBL; AY034643; AAK61483.1; -.
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
NON_TER 356 356
                                                                                                                                                                                             STRAIN=1304;
Huang J.-A., Ficorilli N., Hartley C.A., I
"Polymorphism of open reading frame 71 of
                                                                                                                                                                                                                                                                                           Glycoprotein gp2 (Fragment) Equine herpesvirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telford E.A., Watson M.S., P
Submitted (OCT-1997) to the
EMBL, AF030027; AAC595911;
SEQUENCE 750 AA; 77206 MW
                                                                                                                                                                                                                                                                                                                                                            Q8V0L7
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Telford E.A., Watson M.S., Perry J., Cullina
"The DNA sequence of equine herpesvirus-4.";
J. Gen. Virol. 79:1197-1203(1998).
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCBI_TaxID=10326;
                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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Last annotation updat
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                                                                                  Score 253.5; DB 1
Pred. No. 5.8e-08;
6; Mismatches 142
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Pred. No. 9e-08;
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Matches 81
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Q9N4S7;
01-OCT-2000
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InterPro; IPRO02965; P rich expression.
PRINTS; PRO1217; PRICHEXTENSN.
SEQUENCE 1079 AA; 110532 MW;
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01-JUN-2001 (TrEMBLrel.
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Rhabditidae; Peloderinae;
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EMBL/GenBank/DDBJ
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Pred. No. 3.
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                    Equine herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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Huang J.-A., Ficorilli N.,
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Equine herpesvirus 4.
Viruses; dsDNA viruses, no R
                                                     EMBL; AY034636; AAK61476.1; -. InterPro; IPR000104; Antifreeze 1. PRINTS; PR00308; ANTIFREEZEI.
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01-MAR-2002
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STRAIN=R19/68;
Huang J.-A., Ficorilli N.,
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01-MAR-2002
                                                                                                                                                      Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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PR00308; ANTIFREEZEI.
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Pred. No. 1.8e-07;
1; Mismatches 111;
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RESULT 15
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AC Q8VOM
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DT 01-MA
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RR SHBLI;
DR Inter
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Best Local Similarity
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Q8V0M0;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seque
01-JUN-2002 (TrEMBLrel. 21, Last annot
Glycoprotein gp2 (Fragment).

Gquine herpesvirus 1.

Viruses daDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
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PRINTS; PR00308; ANTIFREEZEI.
NON_TER 389 389
                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AY034640; AAK61480.1; -.
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        Huang J.-A., Ficorilli N., Hartley C.A., F "Polymorphism of open reading frame 71 of
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            and EHV1
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=1070/94;
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333
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                                                                                                                                    115 DSAAMEIQTTQPAATEAQTTPLAATEAQTTRLT-----ATEAQTTPLA-----AT
                                                                                                                                                               157 PITTTPTSTTTTTATT--TVPTTASTTTDTTTAATTTAATTTAATTTAATTTAAT
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                                                     PETEPPEMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLST
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AAW26183	AAW26184	AAW26185	AAY29768	AAW53323	ABB65879	AAW26186	AAW26187	AAW26188	AAY29770	AAY29767	AAW53322	AAG77946	AAY29766	AAW53321	AAY29769	AAW53324	AAY29771	AAY29776	AAW10530	AAY29773	AAY29772	AAU79654	AAY29777	AAY29775	AAY29774	AAR85076	AAR53966	ABB04668	AAW83012	AAW81967	AAY29778	AAW56346	269	AAR53965
#9 of P	#10 of	ent #11 of P	se1	ij	la melan	#12 of	#13 of	世世	ectin ligand	P-8e	gand	er		Ctin	£1	_	_	-	<u></u>	بر	ctin lig	ᢐ	5	'n	5	Ľin	in li	Н,	placenta P-	ש	Human P-selectin l	P-selectin ligand	Human glycoprotein	P-selectin ligand.

# ALIGNMENTS

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/label= N-glycosylation_site	Modified-site 292294			/label= N-glycosylation_site	Modified-site 6567			/label= Tyr-sulfation_site				_ (		/label= Extracellular domain			tide 121	_		Homo sapiens.		P-selectin ligand; adhesin; cell adhesion; antiinflammat		P-selectin ligand.		01-MAR-1996 (first entry)		AAR85075;		5075 AAR85075 standard; Protein; 402 AA.	E7 1

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28-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                fucosyltransferase gene,
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                                                                                                                      APDHISVKQCLLAILILALVATIFFVCTVVLAVRLSRKGHMYPVRNYSPTEMVCISSLLP
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Veldman
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AAW26174

standard; protein; 402

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This sequence represents the human P-selectin glycoprotein ligand-1 (C (PSGL-1). P-selectin is a calcium-dependent carbohydrate binding protein CC expressed on the surfaces of activated platelets and endothelium in CC response to thrombin and other agonists. PSGL-1 is a high affinity CC P-selectin ligand produced by leukocytes. Binding of P-selectin to CC PSGL-1 is calcium ion dependent and is abolished by treatment of the C1 ligand with sialidase. PSGL is a homodimer, which a highly extended CC extracellular domain, which is a feature of mucin-like proteins. This sequence is targeted by the sulphated glycosylated peptides of the CC invention (see AAWS6175-W26188). PSGL-1 is also targeted by the CC invention (see AAWS6175-W26188). PSGL-1 is also targeted by the CC used for inhibiting the binding of P-selectin and other selectins to PSGL-1. They can be used for the treatment of inflammation, injury CC resulting from ischaemia and reperfusion, bacterial sepsis and CC disseminated intravascular coagulation, adult respiratory distress syndrome, tumour metastasis, rheumatoid arthritis, atherosclerosis and other autoimmune or inflammatory disorders. The products can also be used in the production of antibodies and in diagnostic annitations.
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03-AUG-1995;
15-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                        New O-glycan(s) derived from P-selectin glyco:protein (PSGL)-1 - used for inhibiting binding of PSGL-1 to se
                                                                                                                                                                                                                                                                                                                               Claim
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309..333
/note= "transmembrane domain"
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Matches 402
25-APR-1995;
23-OCT-1992;
26-AUG-1993;
22-OCT-1993;
                                                                                                                                                                                                                                                                Human; glycoprotein; P-selectin ligand protein; inflammatory disease; intracellular domain; E-selectin-mediated intercellular adhesion.
                                                                                                                                                                                                                                                                                             Human
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93WO-US10168.
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30-SEP-1994;
07-JUN-1995;
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G, Veldman
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Pred. No. 2.3e-149;
0; Mismatches 0;
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CC having PSL activity which comprises a carbohydrate and a protein. The CC protein includes amino acids 42-60 of AAW72695, but lacks the CC protein includes amino acids 42-60 of AAW72695, but lacks the CR protein includes amino acids 42-60 of AAW72695, but lacks the CC protein includes amino acids 42-60 of AAW72695, but lacks the compression of mature CC protein may be useful in treating conditions characterized by P- or CC protein may be useful in treating conditions characterized by P- or CC protein mediated intercellular adhesion. Such conditions include mycocardial infarction, bacterial or viral infection, metastatic conditions, inflammatory disorders, asthma, emphysema, thermal injury, CC multiple sclerosis, diabetes, Reynaud's syndrome, neutrophilic CC dermatosis, Grave's disease, glomerulonephritis, gingivitis, Crohn's CC periodontitis, haemolytic uremic syndrome, ulcerative colitis, Crohn's CC disease, necrotising entercolitis, and cytokine-induced toxicity. The CC disease, necrotising entercolitis, such and cytokine-induced toxicity. The CC prepare organs for transplantation and to quell organ transplant to CC rejection. The isolated PSL may be used to treat haemodialysis and collection and to great the may also be used to treat haemodialysis and collection.
leukophoresis patients. Additionally, isolated PSL protein may be used an antimetastatic agent. The isolated PSL protein may be used itself as an inhibitor of P- or E-selectin-mediated intercellular adhesion or to design inhibitors of P- or E-selectin-mediated intercellular adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble P-selectin ligand glycoprotein - sequence lacking intracellular domain
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The present sequence represents a P-selectin ligand protein. The extracellular domain
                                                                                                         New isolated DNA encoding fusion protein including P-selectin ligand fragment - to direct second component, e.g. cytokine, to sites of selectin expression, used e.g. to stimulate bone and cartilage
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Matches 402
                                     Human; P-selectin ligand; glycoprotein; fusion protein; infection; inflammation; intercellular adhesion; ulcerative colitis; asthma; diabetes; transplant rejection; myocardial infarction; thermal ini) metastatic condition; autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; neutrophilic dermatosis; Sweet's syndrome; Grave's disease; glomerulonephritis; gingivitis; periodontitis; Crohn's disease; necrotising enterocolitis.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New P-selectin ligand fusion proteins, used for treating e.g. inflammation, infections, asthma, diabetes, ulcerative colitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Pred. No. 2.3e-149;
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Mismatches
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Best Local Similarity
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22-OCT-1993;
28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a novel human P sel which can be used in screening assays for in E-selectin-mediated intercellular adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang
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23-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Column 48-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding P-selectin ligand protein - useful for producing
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N-PSDB; AAV64997.
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Veldman GM;
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Pred. No. 2.3e-149;
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23-OCT-1992;
26-AUG-1993;
22-OCT-1993;
28-APR-1994;
30-SEP-1994;
        A method has been developed for inhibiting P-selectin-mediated binding. The method comprises administering a soluble P-selectin ligand glycoprotein which lacks the transmembrane or intracellular domain of the mature glycoprotein and in which the protein portion comprises at least amino acids 42-60 i.e. Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro, and the carbohydrate portion comprises sialyl Lewis X or sialyl Lewis A. Isolated P-selectin ligand protein may be useful in treating conditions characterised by P- or E-selectin mediated intercellular adhesion. Such conditions include myocardial infarction, bacterial or viral infection, metastatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; promyelocyte; placenta; P-selectin ligand glycoprotein; inflammatory disease; P-selectin-mediated intercellular adhesi E-selectin-mediated intercellular adhesion.
                                                                                                                                                                                                                                                                 Camphausen
Sako DS,
 conditions,
                                                                                                                                                            Claim 1;
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DB; AAV69835.
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                                                                                                                                                         Column 47-50; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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 inflammatory disorders, thermal injury,
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92US-0965662.
93US-0112608.
93WO-US10168.
94US-0235398.
94US-0313305.
95US-0472576.
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                                                                                                                                                                                                   Human; P-selectin glycoprotein ligand-1; PSGL-1; anionic protein purification; immunoglobulin domain; DNA/histone DNA-protein interaction; sulphated protein.
                                                                                                                                               Key
                          Region
                                                     Protein
                                                                                Cleavage-site
                                                                                                          Domain
                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         charged molecules, and purifying, under conditions such that the impurities are not bound to or washed off the substrate. The sample is then dissociated, while the target protein remains bound. The method is useful for isolating and purifying highly anionic target proteins e.g. sulphated proteins, from proteinaceous and non-proteinaceous impurities, purifying highly the protein of the protein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coffman JL,
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                                                                                                                                                                                                                                                             The present invention relates to methods and compositions for modulating stenosis or restenosis in a subject having vascular injury or cardiovascular disease. The method comprises administering a P-selectin antagonist such as soluble P-selectin glycoprotein ligand-1 (PSGL-1) to the subject. The method is useful for preventing, inhibiting or treating stenosis or restenosis in a subject, preferably human, having vascular injury or coronary artery disease. Restenosis is characterised by
                        modulating leukocyte recruitment, inhibiting cell adhesion to blood sequence represents human PSGL-1.
                                                                             constrictive vascular remodelling or neointimal formation. The vascular injury or cardiovascular disease affects a coronary artery, or peripheral artery, preferably a carotid artery. The vascular injury results from angioplasty (percutaneous transluminal coronary angioplasty (PTCA)), or implantation of a stent or stents. The method is also useful for implantation glukocyte recruitment, inhibiting cell to cell adhesion, or including the coronary angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating stenosis or restenosis in subject having vascular injury or cardiovascular disease, comprises administering P-selectin antagonist
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                                                                                                                                                                                                                                                                       intercellular adhesion; promyelocyte; HL60; pM alpha-1,3/alpha-1,4-fucosyltransferase; PACESOI paired basic amino acid converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis in a subject comprising administering a composition comprising an effective amount of a P-selectin antagonist. The polypeptides and polynucleotides of the invention have thrombolytic, and anticoagulant activity. The method is useful for treating or inhibiting thrombosis in subject, particularly a human. The method is also useful for inhibiting cell adhesion to blood vessels in a subject, increasing the movement of cells relative to blood vessels in a subject, or inhibiting the effect a thrombus-inducing agent in a subject. The subject is at risk for thrombosis, e.g. a subject suffering from a cardiovascular disease or disorder (e.g. atherosclerosis or hypertension), or a subject who has undergone cardiovascular or general vascular procedures or intervention
                                                                                                                                       Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          P-selectin ligand
                            Misc-difference
                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR53965 standard;
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                                                                                      /label=
21..310
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                                                                                                                                                                  Location/Qualifiers
                                                         /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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Pred. No. 2.3e-149;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                               PACESOL;
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note=

"potential sulfation site"

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Query Match
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Matches 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA of sequence AAQ63953, encoding P-selectin ligand, was derived from promyelocyte line HL60 clone pMT21:PL85. The ligand comprises residues 1-402, 1-310 (sol.), 42-402 (mature) or 42-310 (sol.) mature) of sequence AAR53965. An allelic variant (AAQ63954, AAR53966) was derived from human placenta. Co-transfection of a mammalian host cell with DNA encoding residues 42-310, plus DNA encoding collaba-1,3/alpha-1,4-fucosyltransferase and DNA encoding a soluble form of a paired basic amino acid converting enzyme (PACESOL), encoded by sequence AAQ63957, allowed production of sol. mature P-selectin ligand glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1994
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26-AUG-1993;
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93US-0112608.
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                     Score 2022; DB 15;
Pred. No. 9.5e~149;
1; Mismatches 1;
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CC The present sequence represents a human glycoprotein having P-selectin CC ligand (PSL) activity. The present invention describes a glycoprotein CC having PSL activity which comprises a carbohydrate and a protein. The CC protein includes mino acids 42-60 of AAW72695, but lacks the CC protein includes mino acids 42-60 of AAW72695, but lacks the CC protein may be useful in treating conditions characterised by P- or CC pSL protein may be useful in treating conditions characterised by P- or CC pSL protein mediated intercellular adhesion. Such conditions include CC myocardial infarction, bacterial or viral infection, metastatic CC conditions, inflammatory disorders, asthma, emphysema, thermal injury, CC dermatosis, diabetes, Reynaud's syndrome, neutrophilic CC dermatosis, Grave's disease, glomerulonephritis, gingivitis, Crohn's CC disease, necrotising enterocolitis, and cytokine-induced toxicity. The isolated PSL protein may also be useful in organ transplantation, both to prepare organs for transplantation and to quell organ transplant CC rejection. The isolated PSL may be used to treat haemodialysis and C1 eukophoresis patients. Additionally, isolated PSL protein may be used as an inhibitor of P- or E-selectin-mediated intercellular adhesion or to design inhibitors of P- or E-selectin-mediated intercellular adhesion.
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23-OCT-1992;
26-AUG-1993;
22-OCT-1993;
22-OCT-1993;
28-APR-1994;
30-SEP-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; glycoprotein; P-selectin ligand protein; inflammatory dise intracellular domain; E-selectin-mediated intercellular adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 49-52; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble P-selectin ligand glycoprotein - with truncated protein sequence lacking intracellular domain
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                                          New isolated DNA encoding fusion protein including P-selectin ligand fragment - to direct second component, e.g. cytokine, to sites of selectin expression, used e.g. to stimulate bone and cartilage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a P-selectin ligand protein. The p-selectin ligand is a glycoprotein. The protein binds in a calcium-dependent manner to P-selectin which is present on the surface of cells. The P-selectin ligand can be used to treat a wide variety of conditions characterised by intercellular adhesion involving P-, E- or L-selectins, e.g. myocardial infarction, infections, metastases, inflammation, Crohn's disease, and to prevent transplant rejection. It can also be used to raise specific antibody (useful therapeutically as inhibitors of adhesion or for immunodiagnosis of inflammation and cancer) or to screen for selective inhibitors. Fusion proteins of the P-selectin expression, e.g. fusion with interleukin-11 to treat bone marrow endothelial cells to stimulate megakaryocyte progenitors, bone morphogenic protein (BMP) to stimulate bone or cartilage formation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                AQTTQPTATEAQTTPLAAMEALSTEPSATEALSMEPTTKRGLFIPFSVSSVTHKGIPMAA
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 EMVCISSILPDGGEGPSATANGGLSKAKSPGLTPEPREDREGDDLTLHSFLP
                                                                  SNLSVNYPVGAPDHISVKQCLLAILILALVATIFFVCTVVLAVRLSRKGHMYPVRNYSPT
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Pred. No. 3
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Human

Human; P-selectin ligand; glycoprotein; fusion protein; infection; inflammation; intercellular adhesion; ulcerative colitis; asthma; diabetes; transplant rejection; myocardial infarction; thermal inj; metastatic condition; autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; neutrophilic dermatosis; Sweet's syndrome; Grave's disease; glomerulonephritis; gingivitis; periodontitis; Crohn's disease; necrotising enterocolitis.

WO9943834-A2

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CC comprising amino acids 42-60, 42-40, 42-310, 42-810 proteins or 42-189

CC of the P-selectin ligand protein. The fusion proteins comprising a

CC P-selectin ligand act as ligands for P-selectin on human endothelial

CC cells and platelets. The isolated P-selectin ligand proteins may be

CC useful in treating conditions characterized by P-, E- or L-selectin

CC mediated intercellular adhesion e.g. myocardial infarction, bacterial

CC or viral infection, metastatic conditions, inflammatory disorders,

CC thermal injury such as burns or frostbite, autoimmune thyroiditis,

CC experimental allergic encephalomyelitis, multiple sclerosis, multiple

CC organ injury syndrome secondary to trauma, diabetes, Reynaud's syndrome,

CC experimental ermatosis (Sweet's syndrome), inflammatory bowel disease,

CC organ injury syndrome, ulcerative colitis, periodontitis,

CC neutrophilic dermatosis (Sweet's syndrome), inflammatory bowel disease,

CC necrotising enterocolitis, granulocyte transfusion associated syndrome,

CC necrotising enterocolitis, granulocyte transfusion associated syndrome,

CC or cytokine-induced toxicity. Isolated P-selectin ligand proteins may

CC also be useful in organ transplantation, both to prepare organs for

CC transplantation and to quell organ transplant rejection. P-selectin

CC patients or used as an antimetastatic agent. The fusion proteins can

CC which the P-selectin ligand protein is fused. The fusion proteins can

CC used for the production of antibodies for use in therapy detection.
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Best Local Similarity
Matches 402; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for the production of antibodies for use in therapy, detection, diagnosis and drug screening. The present sequence represents the human P-selectin ligand protein, as given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 110-111; 145pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Camphausen R,
Larsen GR, S
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ko DS, Shaw G, Veldman GM;
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Pred. No. 3.4e-148;
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88, 42-118 or 42-189
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                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     which can be used in 
E-selectin-mediated
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22-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding P-selectin ligand
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Veldman GM;
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93US-0112608.
93WO-US10168.
94US-0235398.
94US-0316305.
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                                                                                                                                                                                                                                                                                                                                                                                                                                resents a novel human P selectin ligand glycoprotein in screening assays for inhibitors of P- or intercellular adhesion. The protein can be used
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	Search completed: July 14, 2003, 06:12:23 Job time : 77 secs	Search completed: Job time : 77 secs	Sea Job
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2: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptcodata/1/pubpaa/US07_PUBCOMB.pep:*

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9 US-09-994-064-6

9 US-09-994-064-6

10 US-09-815-242-10932

10 US-09-815-242-10932

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Sequence 1, Appli
Sequence 2, Appli
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Sequence 36047, A
Sequence 1068, Ap
Sequence 1068, Ap
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Sequence 6, Appli
Sequence 66, Appli
Sequence 10932, A
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Sequence 10934, Ap
Sequence 108, Appl
Sequence 143, App
Sequence 143, App
Sequence 341, App
Sequence 58, Appl
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## ALIGNMENTS

RESULT 1 US-10-163-853-1

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Publication No. US20030050450A1

GENERAL INFORMATION:

APPLICANT: Coffman, J.L., et al.

TITLE OF INVENTION: Methods for Purifying Highly Anionic Proteins

FILE REFERENCE: 01997.008800

CURRENT APPLICATION NUMBER: US/10/163,853

CURRENT FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: 60/296,402

PRIOR APPLICATION NUMBER: 60/296,402

PRIOR FILING DATE: 2001.06-05

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.1
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Best Local S
Matches 402
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LENGTH: 402
TYPE: PRT
ORGANISM: homo sapiens
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RESULT 3
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US-10-211-786-2
Sequence 1, Application US/09819157
Patent No. US20020132991A1
GENERAL INFORMATION:
APPLICANT: Coffman, J.L., et al.
TITLE OF INVENTION: METHODS FOR PURIFYING HIGHLY ANIONIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MODULATION OF LEUKOCYTE-ENDOTHELIAL INTERACTIONS FOLLOWING ISCHEM FILE REFERENCE: 8702.0099-00000

CURRENT APPLICATION NUMBER: 9002-08-02

PRIOR APPLICATION NUMBER: 60/309,816

PRIOR APPLICATION NUMBER: 60/309,816

PRIOR FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 402
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CURRENT APPLICATION NUMBER: US/09/819,157
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/193,351
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 1
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US-10-211-786-4
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                                                                                                                                                                                 SEQ ID NO 4
LENGTH: 313
TYPE: PRT
                                                      Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10211786
Publication No. US20030083258A1
GENERAL INFORMATION:
APPLICANT: Michael J. Eppihimer
APPLICANT: Robert G. Schaub
APPLICANT: Romald Tuma
TITLE OF INVENTION: MODULATION OF LEUKOCYTE-ENDOTHELIAL INTERACTIONS FOLLOWING ISCHEM
FILE REFERENCE: 8702.0099-00000
CURRENT APPLICATION NUMBER: US/10/211,786
CURRENT FILING DATE: 2002-08-02
CURRENT FILING DATE: 2002-08-02
CURRENT FILING DATE: 2002-08-02
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Best Local S
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PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
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TYPE: PRT
ORGANISM: Homo Sapiens
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                                                        , 68
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               1 MPLQLLLLLLLGPGNSLQLWDTWADEAEKALGPLLARDRRQATEYEYLDYDFLPETEPP
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                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGGEGPSATANGGLSKAKSPGLTPEPREDREGDDLTLHSFLP 402
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nilarity 97.8%;
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                                                      Score 465; DB 9
Pred. No. 1e-25;
0; Mismatches
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SEQ ID NO 36047
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                                                                 TYPE: PRT
ORCANISM: Homo sapiens
PEATURE:
PEATURE:
OTHER INFORMATION: MAP TOTHER INFORMATION: EXPRE
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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                   OTHER INFORMATION:
OTHER INFORMATION:
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00666
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   INFORMATION:
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Chen, Wensheng
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               MAP TO AB023048.1
EXPRESSED IN PLACE
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            IN HBL100, SIGNAL = 1.4
IN HEART, SIGNAL = 1.5
IN PETAL LIVER, SIGNAL = 1.5
IN ADULT LIVER, SIGNAL = 1.5
IN HELA, SIGNAL = 1.1
   BRAIN,
                                                                                                    PLACENTA,
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CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
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Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                  Query Match
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Best Local
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115 DSAAMEIQTTQPAATEA-QTTPLAATEAQTTRLTATEAQ---TTPLAATEAQTTPPAATE
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                                                                                                                                                                                                                                                                                                                                                  T: Carter, Darrick
INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
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                                                                   PETEPPEMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLST
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Vedvick Thomas S.
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Skeiky, Yasir A. W.
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Benson, Darin R
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Wang, Aijun
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                                                                                                    Score 196.5; I
Pred. No. 3.9e-
24; Mismatches
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BONE MARROW, SIGNAL
BT474, SIGNAL = 1.4
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US-09-922-217-1068
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US-09-922-217-1068
                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
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    VTPTPTPTGTQTPTTTPTTTTTTTVTP-----TPTPTGTQTPTTTPTTTTTTTTTTPTPTP 4190
                                                                                                                 DSAAMEIQTTQPAATEA-QTTPLAATEAQTTRLTATEAQ----TTPLAATEAQTTPPAATE
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                                                          TSRS-----TSSPLTESTTLLSTLPPAIEMTSTAPPSTPTAPTTTSGGHTLSPPPSTT
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Smith, Carole Lynn
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Benson, Darin R.
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                                                                                                                                                                                                                         Score 196.5; DB 10; Length 5179;
Pred. No. 3.9e-05;
'4; Mismatches 169; Indels 81;
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RESULT 9
US-09-994-064-6
; Sequence 6, Application US/09994064
; Publication No. US20030082788A1
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US-09-833-263-1068
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FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1068
LENGTH: 5179
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Meagher, Madeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 9.7%; Score 196.5; DB 10; Local Similarity 24.5%; Pred. No. 3.9e-05; 1es 89; Conservative 24; Mismatches 169;
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                                              335 LSRKGHMYPVRNYSP-TEMVCISSLLPDGGEGPS-----
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Stolk, John A.
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-TSSPLTESTTLLSTLPPAIEMTSTAPPSTPTAPTTTSGGHTLSPPPSTT
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                                                    ---ATANGGLSKAKSPGLT 383
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-994-064-6
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Best Local
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
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CURRENT APPLICATION DATA:
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APPLICANT: Cochran, Marl
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APPLICATION NUMBER:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                     686 QNPTSSGTGTHNTEPRTYPVQTTPH 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                PLAATEA-----QTTPPAATEAQTTQPTGLEAQTTAPAAM------EAQTTAPA 197
                                                                                                                                                                                                                                                                                                                                                                        LSTDSAAMEIQT----TQPAATEAQT---TPLAATEAQTTRLTATEAQT---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGATLPPFDTAAPDFDTGTSPTPTTVPEPAITTLIPRSTSDMGFFSTARATGSETL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGNSLQLWDTWADE-----AEKALGPLLAR-----DRRQATEYEYLDYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                          SNLSVN----
                                                                                                             EPEVLTQSPSTEPVPFTRTLGAEPEITQTPSAAPEVYTRSSSTMPETAQST----PLAS
                                                                                                                                                QP-TATEAQTT-PLAAMEALSTEPSATEALSMEPT--TKRGLFIPFSVSSVTHKGIPMAA 290
                                                                                                                                                                                   TTLSSSTEPAIFTRTQSAGTEAFTQTSSAEPDTMRTQSTETHFFTQAPSTVPKATQTPST
                                                                                                                                                                                                                                                             PGAETEAPAQTPSTIPEIFTQSRSTPPETARAPSAAPEVFTQSSSTVTEVFTQTPSTVPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mark D.
RECOMBINANT INFECTIOUSLARYNGOTRACHEITIS VIRUS
AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/468,190
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                                                                          -YPVGAPDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 195; DB 9;
Pred. No. 6.9e-06;
8; Mismatches 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
                                                                        304
                                                                                                                                                                                                                        --- AMEAOTTOTTAM-EAOTTAPEATEAOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 985;
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                                                                                                                                                                                                                        234
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US-09-994-064-66
; Sequence 66, Application US/09994064
; Publication No. US20030082788A1
; GENERAL INFORMATION:
uild Martha A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUSLARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/994,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                   394 --- SVPVQETDRTLSTTPLTLPLTPGESENTLFPTTAPGISTETPSAAHETTQTQSAETV 450
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291
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SNLSVN----
                                                                                                                                              AMEAOTTPPA-------AMEAOTTOTTAM-EAOTTAPEATEAOTT
                                                                                                                                                                                                                        PLAATEA-----QTTPPAATEAQTTQPTGLEAQTTAPAAM-----
                                                                                                                                                                                                                                                             VFTQSPSTESETARSQSQEPWYFTQTPSTEQAALTQTQIAETEALFTQTPSAEQMTFTQT
                                                                                                                                                                                                                                                                                                                                                                        LPETEPPEMLRNSTDTTPLTGPGTP--ESTTVEPAARRSTGLDAGGAVTELTTELANMGN 111
                                                                                                                                                                                                                                                                                                                                                                                                             PGATLPPFDTAAPDFDTGTSPTPTTVPEPAITTLIPRSTSDMGFFSTARATGSETL----
                                   EPEVLTQSPSTEPVPFTRTLGAEPEITQTPSAAPEVYTRSSSTMPETAQST-----PLAS
                                                                        QP-TATEAQTT-PLAAMEALSTEPSATEALSMEPT--TKRGLFIPFSVSSVTHKGIPMAA
                                                                                                           TTLSSSTEPAIFTRTQSAGTEAFTQTSSAEPDTMRTQSTETHFFTQAPSTVPKATQTPST
                                                                                                                                                                                   PGAETEAPAQTPSTIPEIFTQSRSTPPETARAPSAAPEVFTQSSSTVTEVFTQTPSTVPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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-YPVGAPDH 304
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Pred. No. 6.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138;
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RESULT 12
US-09-801-368-108
; Sequence 108, Application US/09801368
; Patent No. US20020128250A1
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Best Local Similarity
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Sequence 10932, Application US/09815242
Patent No. US20020061569A1
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                        855
                                                                                                                                                                                                                                                                             169 ТЕАСТТСРТСЬЕАСТТАРААМЕАСТТАРААМЕАСТТРРААМЕАСТТСТТАМЕАСТТАРВА 228
                                                                                                                                                                                                                                                                                                                            795
                                                                                                                                                                                                                                                                                                                                                                     109 MGNLSTDSAAMEIQTTQPAATEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAA 168
                                                                                                                                                                                         229 TEAQTTQPTATE-----AQTTPLAAMEALSTEPSATEALSMEPTTK 269
                                                                                                                                                                                                                                                                                                                                                                                                                735 ALLLLVEKSTETTSNTSESSTSSTTSESSSTSESSTSSTTNESSSTSESSTSESSTTNESSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EML---RNSTDTTPLTGPGTPESTTVEPAARRSTGLD------AGGAVTELTTELAN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                  TSESSTPSTLNENSQSKGQNSVIYAVES-NQDPNDAQSNS-KPSAK 958
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Trawick, John D.
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Pred. No. 1.8e-05;
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/2180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 9/632,366
PRIOR APPLICATION NUMBER: US 9/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 PAAMEAQTTPPAAMEAQTTQTTAMEAQTTAPEATEAQTTQPTA--TEAQTTPLAAMEALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 TEPSATEALSMEPTTKRGLFIPFSVSSVTHKGIPMAASNLSVNYPVGAP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 SSTSESSTSSSTTAPATPTTTSCTKEKPTPPTTTSCTKEKPTPPHHDTT-PCTKKKTTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 LAATEAQTTRLŢATEAQTŢPLAAŢEAQTŢPPAAŢEAQTŢQPŢGLEAQŢŢAPAAMEAQŢŢA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 GTKSSTTTSSTSESST---------TTSSTSESSTTTSSTSESSTTT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 GTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTDSAAMEIQTTQPAATEAQTTP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maxon, Mary
Milne, Todd
No. US20020128250Alman, T
Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TESSSAPVTS---STTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hecht, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.2%; Score 187; DB 10; 24.0%; Pred. No. 3.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thea
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666

APPLICATION NUMBER: US 60/236,359

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RESULT 14
US-10-234-432-59
; Sequence 59, Application US/10234432
; Publication No. US20030091598A1
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OTHER INFORMATION: EXPRESSED IN PLACEN
OTHER INFORMATION: EXPRESSED IN HEL100
OTHER INFORMATION: EXPRESSED IN HEART,
OTHER INFORMATION: EXPRESSED IN ADULT
OTHER INFORMATION: EXPRESSED IN HELA,
OTHER INFORMATION: EXPRESSED IN HELA,
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN BONE M.
OTHER INFORMATION: EXPRESSED IN BONE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/774,203 FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                  160 EAQTTPPAATEAQTTQPTGLEAQTTAPAAMEAQTTAPAAMEAQTTPPAAMEAQTTQTTAM 219
                                                                                                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                        220 EAQTTAPEATEAQTTQPTATEAQTTPLAAM----EALSTEPSATEALS---MEPTT 268
                                                                                                                                                                                                                                                                                                                                                                                                                        53 SEPTMASTMGSETTMASTIG-PETTKVSTASSEVTTVFAAGSETIRASTVGSETTTVSTT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 TEPPEMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVT-----ELTTELANM 109
                                                                                                                                               GSETKTAYTTGSETTTASNTGLETTTVFTIGSDTTTASTEGSETTAVSATGSEMTT
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25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 183.5; DB 10;
; Pred. No. 1.2e-05;
51; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN HBL100, SIGNAL = 1.4
IN HEART, SIGNAL = 1.1
IN PETAL LIVER, SIGNAL = 1.5
IN ADULT LIVER, SIGNAL = 1.5
IN HELA, SIGNAL = 1.1
IN HELA, SIGNAL = 2
IN LUNG, SIGNAL = 4.7
IN BONE MARROW, SIGNAL = 2.1
IN BT474, SIGNAL = 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331;
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RESULT 15
US-10-121-988-143
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; ORGANISM: Babesia
US-10-234-432-59
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; ORGANISM: HSV-2
US-10-121-988-143
                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 210121.560
CURRENT APPLICATION NUMBER: US/10/234,432
CURRENT FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 143, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Homer, Mary
APPLICANT: Lodes, Mich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT: Persing, David H.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: TREATMENT OF BABESIA
                                                                                                                                              CURRENT FILING DATE:
                                                                                                                                                               FILE REFERENCE: 210121.538C1
CURRENT APPLICATION NUMBER: US/10/121,988
                                                                                                                                                                                               APPLICANT: Swanson, Ryan M.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hosken, Nancy Ann
                                        TYPE:
                                                            LENGTH: 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 ---EPSATEALSMEPTTK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ---QTTP-----PAATEAQTTQETGLEAQTTAPAAMEAQTTA-----PAAMEAQTT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 PQQPAQVAPQATAGIQQAQPQPVATETATAEQPVAATTTEVQ-MPQAAAESPAPILETPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 QAT-----DVAPSSDQP---TQDAQQAPSPNP-TPASTVATPEASQGSANQQQSQTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 QATEYEYLDYDFLPETEPPEMLRNSTDTTPLTGPGTPESTTVEPAA-----RRSTGLDA
                                                                                                                                                                                                                                                                                   McGowan, Patrick
Sleath, Paul R.
Mossman, Sally P.
Evans, Lawrence S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPAAMEAQT----TQTTAMEAQTTAPEATEAQTTQPTATEAQTTPLAAMEALST-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAVTELTTELANMGNLSTDSAAME-----128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPPVQTAQTRPVAQPQVVVAEAQVVQPPVKAAQ-AQPVVKDQAAQPVASVAPQATAGIQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10121988
5. US20030068327A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                     Windows Version
                                                                                                                                              2002-04-11
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Search completed: July 14, 2003, 06:22:20 Job time : 71 secs
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                                                                                           644 TASPALDILPIISTTIHTAAFVCLVALAAQLWRGRAGRRRYAHPSVRY-----VCL 694
                                                                                                                                                                                                                                         253 STEPSATEALSMEPTTKRGLFIPFSVSSVTHKGIPMAASNLSVNYPVG-APDHISVKQCL 311
                                                                                                                                                                                                                                                                                          529 RTPPTDPKTHPHGPADAPPGSPAPPPPEHRGGPEEFEGAGDGEPPEDDDSATGLAFRTPN 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 PPATASVESSPLPAAAAATPGAGHTNTSSASAAKTP-PTTPAPTTPPTTSTHATPRPTTP 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 DTTPLTGPGTPESTTVEPAARRSTGLDAGGAVT---ELTTELANMGNLSTDSAAMEIQTT 124
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11 Similarity 22.8%; Pred. No. 9.6e-05; 
95; Conservative 49; Mismatches 167; Indels 105; Gaps
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Result
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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US-08-477-254A-2
US-08-428-734B-2
US-08-428-734B-2
US-09-063-237-1
US-08-472-576B-4
US-08-477-254A-4
US-08-477-254A-4
US-08-4713-556F-42
US-08-713-556F-42
US-08-713-556F-36
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US-07-757-022B-44	US-07-757-022B-104	US-07-757-022B-58	US-07-757-022B-74	US-07-757-022B-84	US-07-757-022B-14	US-08-928-361B-17	US-08-700-651-12	PCT-US95-04611A-19	US-09-328-599A-1	US-08-783-774-2	US-09-171-699-10	US-08-276-967-2	PCT-US95-10661A-6	US-08-296-791-6	PCT-US95-09941-2	US-08-287-001A-2	US-09-556-706B-2
Sequence 44, Appl	Sequence 104, App	Sequence 58, Appl	Sequence 74, Appl	Sequence 84, Appl	-	•	Sequence 12, Appl	Sequence 19, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 10, Appl	•	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli

## ALIGNMENTS

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Sequence 2, Application
; Patent No. 5840679
; GENERAL INFORMATION:
APPLICANT: Larsen,
APPLICANT: Chang, b)
APPLICANT: Veldman
APPLICANT: Veldman
APPLICANT: Veldman
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US-08-472-576B-2
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TELEFAX: (617) 876-8851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                   APPLICANT: Camphausen, Raymond
TITLE OF INVENTION: NOVEL P-SEI
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                            SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                        STREET:
CITY: CP
STATE: N
COUNTRY:
FILING DATE:
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Cumming, Dale
Kumar, Ravindra
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Chang, Xiao Jia
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              US/08/472,576B
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Pred. No. 1.9e-173;
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RESULT 3 US-08-428-734B-2

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Sequence 2, Application US/08428734B Patent No. 5843707 GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Larsen, Glenn Sako, Dianne Chang; Xiao Jia Veldman, Geertru

Geertruida

Glenn

APPLICANT:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,398
FILING DATE: 28-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,305
FILING DATE: 30-SEP-1994

PRIOR APPLICATION NUMBER: US 08/316,305
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI 5213E-FC
REFERENCE/DOCKET NUMBER: GI 5213E-FC
TELEPONE: (617) 498-8224
TELEPAX: (617) 498-8224
TELEPAX: (617) 676-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 402;
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 22-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTILING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/112,608
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 23-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
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DGGEGPSATANGGLSKAKSPGLTPEPREDREGDDLTLHSFLP
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,305
PILING DATE: 30-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: BROWN, SCOTT A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/215 200
FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Kumar, Ravindra
APPLICANT: Shaw, Gray
APPLICANT: Camphausen, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/112,608
FILING DATE: 26-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/1016
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APPLICATION NUMBER: US 0:
FILING DATE: 23-OCT-1992
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
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AQTTPLAAMEALSTEPSATEALSMEPTTKRGLFIPFSVSSVTHKGIPMAASNLSVNYPVG
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87 CAMBRIDGEPARK DRIVE
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US-09-063-237-1
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Matches
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Sequence 1, App....
                                                                                                                                                                                                                                                       Query Match
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APPLICANT: MCEYER, Rodger P.
APPLICANT: Cummings, Richard D.
APPLICANT: Cummings, Richard D.
TITLE OF INVENTION: O-Glycan Inhibitors of Selectin Mediated
TITLE OF INVENTION: Inflammation Derived from PSGL-1
                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (404)873-8794
TELEPAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 30306-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/063,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    Local Similarity
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Y: US
                   IQTTQPAATEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAATEAQTTQPTGLE
                                                                       EMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTELTTELANMGNLSTDSAAME
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IQTTQPAATEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAATEAQTTQPTGLE
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                                                                                                                                                                                                                                                                                                                                                                                  402 amino acids
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2800 One Atlantic Center, 1201 West Peachtree
                                                                                                                                                                                                               100.0%; Score 2030; DB 3; ilarity 100.0%; Pred. No. 1.9e-173; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                     Length 402;
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US-08-713-556F-2
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APPLICANT: Shaw, Gray
TITLE OF INVENTION: N
NUMBER OF SEQUENCES:
       REFERENCE/DOCKET NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPRONE: (617) 498-8224
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APPLICANT:
                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/10168 FILING DATE: 22-OCT-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,556F
                                                                                                                                 PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US 08/428,734
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APPLICATION NUMBER:
FILING DATE: 26-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOTT A.
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APPLICATION NUMBER: US 08/316,305
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ZIP: 02140
   TELEFAX:
                                                                     NAME: BROWN, SCOTT I
REGISTRATION NUMBER:
                                                                                                                         FILING DATE:
                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 28-APF
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87 CAMBRIDGEPARK DRIVE
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Cumming, Dale
Kumar, Ravindra
Shaw, Gray
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Sako, Dianne
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US-08-477-254A-4
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Best Local Sim
Matches' 402;
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APPLICANT: Larsen,
APPLICANT: Sako, D
APPLICANT: Chang,
APPLICANT: Veldman
APPLICANT: Cumming
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Patent No.
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                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIA Release #1.0, 1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,254/
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TOPOLOGY: linear
MOLECULE TYPE: protein
                CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                       TITLE OF
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APPLICATION NUMBER:
                                                    FILING DATE:
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                CITY:
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o. 5827817
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Sako, Dianne
Chang, Xiao Jia
Veldman, Geertru
Cumming, Dale
Kumar, Ravindra
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Shaw, Gray
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                                                                                                     Release #1.0,
 US 07/965,662
                                                                       US/08/477,254A
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                                                                                                         Version
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RESULT 7
US-08-472-576B-4
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APPLICATION NUMBER: US 08/235,398
FILLING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,305
FILLING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REGISTRATION NUMBER: GI 5213E-PC
REGISTRATION NUMBER: GI 5213E-PC
REGISTRATION NUMBER: GI 5213E-PC
TELEPHONE: (617) 498-8224
TELEPAN: (617) 896-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TORNEY SECONDATION ACIDS
TORNE
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                       GENERAL INFORMATION:
APPLICANT: Larsen;
APPLICANT: Chang, x
APPLICANT: Chang, x
APPLICANT: Veldman,
APPLICANT: Cumming,
APPLICANT: Kumar, R
                                                                                                                                                                                                                   Sequence 4, Application US/08472576B Patent No. 5840679
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APPLICATION NUMBER: PCT/US93/10168
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
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  APPLICANT:
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                                                                                            Larsen, Glenn
Sako, Dianne
Chang, Xiao Jia
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                    Veldman, Geertruida
Cumming, Dale
Kumar, Ravindra
Kumar, Ravi
Shaw, Gray
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Pred. No. 4.3e-172;
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Best Local Similarity
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,662
PRIOR APPLICATION NUMBER: US 08/112,608
PRIOR APPLICATION NUMBER: US 08/112,608
APPLICATION NUMBER: US 08/112,608
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10168
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,398
PRIOR APPLICATION NUMBER: US 08/235,398
PRIOR APPLICATION NUMBER: US 08/316,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 876-58:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acid
TYPE: amino acid
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REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI 5'
TELECOMMUNICATION INFORMATION:
TPLEPHONE: (617) 498-8224
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
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NAME: BROWN, SCOTT A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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CITY: CAMBRIDGE
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                         AQTTQPTATEAQTTPLAAMEALSTEPSATEALSMEPTTKRGLFIPFSVSSVTHKGIPMAA 290
                                                                                                   AQTTQPTGLEAQTTAPAAMEAQTTAPAAMEAQTTPPAAMEAQTTQTTAMEAQTTAPEATE
                                                                                                                                                                                      IQTTQPAA-----TEAQTTPLAATEAQTTRLTATEAQTTPLAATEAQTTPPAATE 170
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AQTTQPTATEAQTTPLAAMEALSTEPSATEALSMEPTTKRGLF1PFSVSSVTHKG1PMAA
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(617) 876-5851
(77) TD NO: 4:
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Pred. No. 4.3e-172;
0; Mismatches 0;
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Query Match
Best Local Similarity
Matches 402; Conserv
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GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
                                                                                                                                            TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOTT A.
REGISTRATION NUMBER: 32,72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/112,608
FILING DATE: 26-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10168
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0:
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CAMERIDGEPARK DRIVE
                                                                                           TOPOLOGY: 15
MOLECULE TYPE:
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CLASSIFICATION: 435
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INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN
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Sako, Dianne
Chang, Xiao Jia
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       Conservative
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Shaw, Gray
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Cumming, Dale
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                    99.3%;
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   Score 2015; DB 2;
Pred. No. 4.3e-172;
0; Mismatches 0;
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                                     Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08713556F
Patent No. 6277975
GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
APPLICANT: Sako, Dianne
APPLICANT: Chang, Xiao Jia
APPLICANT: Veldman, Geertruida M.
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                                                    APPLICATION NUMBER: US 07/965,662
PRILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,608
FILING DATE: 26-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10168
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                         FILING DATE:
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR NUMBER: US 07/965,662
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ADDRESSEE: LEGAL AFFAIRS
       PRIOR APPLICATION DATA
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                      APPLICATION NUMBER: FILING DATE: 28-AP
                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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T: Shaw, Gray
INVENTION: NC
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Cumming, Dale
Kumar, Ravindra
                    MBER: US 08/235,398
28-APR-1994
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                                                                                          PCT/US93/10168
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REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             Sequence. 42,
Patent No. 6
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                                                                                                                                                                                                                                                         tent No.
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                                                                                       APPLICANT: Shaw, Gray
TITLE OF INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN
NUMBER OF SEQUENCES: 45
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                           CORRESPONDENCE ADDRESS:
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                  STREET: 8/ CAMBRIDGE
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COUNTRY:
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WGY: linear
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Sako, Dianne
Chang, Xiao Jia
Channe
Chang, Kao Jia
Leithan, Geertruida M
Cumming, Dale
Kumar, Ravindra
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Shaw, Gray
                                                              LEGAL AFFAIRS
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US-08-713-556F-36
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Best Local Similarity
                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                APPLICANT:
APPLICANT:
                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                APPLICANT: Kumar, Ravindra
APPLICANT: Shaw, Gray
TITLE OF INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOTT A.
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APPLICATION NUMBER: US 0
FILING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,662
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 22-OCT-1993
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ADDRESSEE:
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Cumming, Dale
Kumar, Ravindra
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Chang, Xiao Jia
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96.7%;
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RESULT 12
US-08-713-556F-38
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                                                                                                                                      Sequence 38, Application US/08713556F Patent No. 6277975
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                                                                                                    GENERAL INFORMATION: APPLICANT: Larsen,
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                                                                  APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOTT A.
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BROWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI 5213F
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/316,305
FILING DATE: 30-SEP-1994
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/428,734 FILING DATE: 25-APR-1995
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                                                                                                                                                                                                                                                                                                                                    1 MPLQLLLLLILLGPGNSLQLWDTWADEAEKALGPLLARDRRQATEYEYLDYDFLPETEPP
                                                                                                                                                                                                                                                                                                                                                                                 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                              Larsen, Glenn
Sako, Dianne
Chang, Xiao Jia
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(617) 876-5851
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Shaw, Gray
          Veldman, Geertruida
Cumming, Dale
Kumar, Ravindra
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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22-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 465; DB 4;
Pred. No. 8.7e-34;
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                                      RESULT 13
US-08-713-556F-40
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Sequence 40, Application US/08713556F Patent No. 6277975
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Best Local
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FILING DATE: 25-APR-1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10168
FILING DATE: 22-OCT-1993
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APPLICATION NUMBER: US 07/965,662
FILING DATE: 23-OCT-1992
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/235,398
FILING DATE: 28-APR-1994
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                        61 EMLRNSTDTTPLTGPGTPESTTVEPAAR 88
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                                                                                                                                                                                            MPLQLLLLLILLGPGNSLQLWDTWADEAEKALGPLLARDRRQATEYEYLDYDFLPETEPP 60
                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                       EMLRNSTDTTPLTGPGTPESTTVEPAAR 88
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87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                          Conservative
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/ 100.0%; Pr
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GENERAL INFORMATION:

APPLICANT:

Larsen, Glenn Sako, Dianne Chang, Xiao Jia

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PCT-US96-10043-3
                                                                                                              RESULT 14
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                                                               Sequence 3, Application PC/TUS9610043 GENERAL INFORMATION:
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Best Local 9
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INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/316,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOTT A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US93/10168
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,398
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,608
FILING DATE: 26-AUG-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
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Cumming, Dale
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Pred. No. 7.1e-17;
2; Mismatches 2
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PCT-US96-10043-13
; Sequence 13, Application PC/TUS9610043
; GENERAL INFORMATION:
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Best Local Similarity
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PILING LAND CHASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
APPLICATION 14-JUN-1995
                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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REGISTRATION NUMBER:
REFERENCE/DOCKET NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
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APPLICATION NUMBER:
FILING DATE: 14-JUN-
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TYPE: amino acid
STRANDEDNESS: not rele
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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